

PELLICER1A.ST25.txt  
SEQUENCE LISTING

<110> PELLICER, Angel  
LEONARDI, Peter  
INGHIRAMI, Giorgio

<120> HUMAN RGR ONCOGENE AND TRUNCATED TRANSCRIPTS THEREOF DETECTED IN T CELL MALIGNANCIES, ANTIBODIES TO THE ENCODED POLYPEPTIDES AND METHODS OF USE.

<130> PELLICER=1A

<140> NOT YET ASSIGNED

<141> 2003-07-23

<150> 60/397,873

<151> 2002-07-24

<160> 28

<170> PatentIn version 3.2

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<211> 2897

<212> DNA

<213> Homo sapiens

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<221> CDS

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PELLICER1A.ST25.txt

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aggaccaggg gacccagatc tggagcttg atg agg aag ctg ctc aca aat ctg Met Arg Lys Leu Leu Thr Asn Leu	1194
1 5	
cct gca gct gca gtc ttg agt gcc cag gtg tac agt gct gtg ctc cag Pro Ala Ala Ala Val Leu Ser Ala Gln Val Tyr Ser Ala Val Leu Gln 10 15 20	1242
ggc ctt tgg gaa gag aat gtc tgt ggg acg cca ggg cgc acg agg gtc Gly Leu Trp Glu Glu Asn Val Cys Gly Thr Pro Gly Arg Thr Arg Val 25 30 35 40	1290
tgt aca gcc ctg ctg tat ggc cag gtc tgc ccc ttc cag gac agc act Cys Thr Ala Leu Leu Tyr Gly Gln Val Cys Pro Phe Gln Asp Ser Thr 45 50 55	1338
gat ggc tta cgc acc atc acc tcc att ttg ttc aac tgg ccc ccc gaa Asp Gly Leu Arg Thr Ile Thr Ser Ile Leu Phe Asn Trp Pro Pro Glu 60 65 70	1386
aac act tca gtt tac tat cag ccc ccg caa cggtca tct ttc cgg ata Asn Thr Ser Val Tyr Tyr Gln Pro Pro Gln Arg Ser Ser Phe Arg Ile 75 80 85	1434
aag ctg gcc ttc agg aac ctc tcc tgg cct gga ctg ggc ttg gag gac Lys Leu Ala Phe Arg Asn Leu Ser Trp Pro Gly Leu Gly Leu Glu Asp 90 95 100	1482
cat cag gaa att gtc cta ggc cag ttg gtg ctt ccg gag ccc aac gag His Gln Glu Ile Val Leu Gly Gln Leu Val Leu Pro Glu Pro Asn Glu 105 110 115 120	1530
gcc aag cca gat gat cct gct cca cgt cct ggg caa cac gca tta aca Ala Lys Pro Asp Asp Pro Ala Pro Arg Pro Gly Gln His Ala Leu Thr 125 130 135	1578
atg ccg gcc ctg gag cca gca cca cca ctg ctg gcg gac ctg ggg cct Met Pro Ala Leu Glu Pro Ala Pro Pro Leu Leu Ala Asp Leu Gly Pro 140 145 150	1626
gct ctg gag cca gag tca cct gca gcc ctg ggt cca cca gga tat cta Ala Leu Glu Pro Glu Ser Pro Ala Ala Leu Gly Pro Pro Gly Tyr Leu 155 160 165	1674
cat tca gca cca ggg cca gca cca gca cca ggg gaa ggg ccc cct cca His Ser Ala Pro Gly Pro Ala Pro Ala Pro Gly Glu Gly Pro Pro Pro 170 175 180	1722
ggg aca gtg ctg gag cca cag tca gcc cca gag tcc tcc tgt ccc tgt Gly Thr Val Leu Glu Pro Gln Ser Ala Pro Glu Ser Ser Cys Pro Cys 185 190 195 200	1770
cgt ggg tct gta aag aac caa ccc agt gag gag ctg cct gac atg acg Arg Gly Ser Val Lys Asn Gln Pro Ser Glu Glu Leu Pro Asp Met Thr 205 210 215	1818
acc ttc cct ccc agg ctg ctg gca gag cag ctg acc ctc atg gat gcg Thr Phe Pro Pro Arg Leu Leu Ala Glu Gln Leu Thr Leu Met Asp Ala 220 225 230	1866
gag ctg ttc aag aag gtg gtg ctc cac gaa tgc ttg ggc tgc atc tgg Glu Leu Phe Lys Lys Val Val Leu His Glu Cys Leu Gly Cys Ile Trp 235 240 245	1914
ggc caa gga cat ctg aag ggg aat gag cac atg gca ccc aca gtt cgt	1962

## PELLICER1A.ST25.txt

Gly Gln Gly His Leu Lys Gly Asn Glu His Met Ala Pro Thr Val Arg  
 250 255 260

gcc acc atc gca cac ttc aac agg ctc acc aac tgc atc acc acc tcc 2010  
 Ala Thr Ile Ala His Phe Asn Arg Leu Thr Asn Cys Ile Thr Thr Ser  
 265 270 275 280

tgc ctc ggg gac cac agc atg agg gcc cggt gac agg gcc agg gtgt gtgt 2058  
 Cys Leu Gly Asp His Ser Met Arg Ala Arg Asp Arg Ala Arg Val Val  
 285 290 295

gag cac tgg atc aag gtgt gcc agg gag tgc cta agc ctc aac aac ttc 2106  
 Glu His Trp Ile Lys Val Ala Arg Glu Cys Leu Ser Leu Asn Asn Phe  
 300 305 310

tcc tcg gtgt cac gtc atc gtc tct gct ctgt tgc agc aac cca ata ggt 2154  
 Ser Ser Val His Val Ile Val Ser Ala Leu Cys Ser Asn Pro Ile Gly  
 315 320 325

cag cta cac aag acg tgg gca gga gtgt tcc agc aaa agc atg aaa gag 2202  
 Gln Leu His Lys Thr Trp Ala Gly Val Ser Ser Lys Ser Met Lys Glu  
 330 335 340

cta aaa gaa ctc tgc aaa aaa gac act gca gtgt aag agg gac cta ctg 2250  
 Leu Lys Glu Leu Cys Lys Lys Asp Thr Ala Val Lys Arg Asp Leu Leu  
 345 350 355 360

atc aag gcg ggg agc ttt aag gtgt gcc acc cag gag agg aac ccc cag 2298  
 Ile Lys Ala Gly Ser Phe Lys Val Ala Thr Gln Glu Arg Asn Pro Gln  
 365 370 375

aga gtc cag atg agg ctg cgg agg cag aag aag ggt gtgt gtc ccc ttc 2346  
 Arg Val Gln Met Arg Leu Arg Arg Gln Lys Lys Gly Val Val Pro Phe  
 380 385 390

ctg ggg gat ttt ctg act gag tta cag agg ctg gat tcg gcc atc ccg 2394  
 Leu Gly Asp Phe Leu Thr Glu Leu Gln Arg Leu Asp Ser Ala Ile Pro  
 395 400 405

gac gac ctg gat ggc aac acc aac aag agg agc aag gag gtc cga gtt 2442  
 Asp Asp Leu Asp Gly Asn Thr Asn Lys Arg Ser Lys Glu Val Arg Val  
 410 415 420

ctg cag gaa atg cag ctg ctc caa gtgt gct gcc atg aat tac agg ctt 2490  
 Leu Gln Glu Met Gln Leu Leu Gln Val Ala Ala Met Asn Tyr Arg Leu  
 425 430 435 440

cgg cct ctt gag aaa ttt gtc acc tat ttc aca aga atg gag cag ctc 2538  
 Arg Pro Leu Glu Lys Phe Val Thr Tyr Phe Thr Arg Met Glu Gln Leu  
 445 450 455

agt gac aaa gag agc tac aag ctg tcc tgc cag ctg gag ccc gaa aac 2586  
 Ser Asp Lys Glu Ser Tyr Lys Leu Ser Cys Gln Leu Glu Pro Glu Asn  
 460 465 470

ccg taggctggca acatcctgca gtggctggga acccaccggg atgctggcca 2639  
 Pro

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<212> PRT  
<213> Homo sapiens

<400> 2

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20 25 30

Gly Thr Pro Gly Arg Thr Arg Val Cys Thr Ala Leu Leu Tyr Gly Gln  
35 40 45

Val Cys Pro Phe Gln Asp Ser Thr Asp Gly Leu Arg Thr Ile Thr Ser  
50 55 60

Ile Leu Phe Asn Trp Pro Pro Glu Asn Thr Ser Val Tyr Tyr Gln Pro  
65 70 75 80

Pro Gln Arg Ser Ser Phe Arg Ile Lys Leu Ala Phe Arg Asn Leu Ser  
85 90 95

Trp Pro Gly Leu Gly Leu Glu Asp His Gln Glu Ile Val Leu Gly Gln  
100 105 110

Leu Val Leu Pro Glu Pro Asn Glu Ala Lys Pro Asp Asp Pro Ala Pro  
115 120 125

Arg Pro Gly Gln His Ala Leu Thr Met Pro Ala Leu Glu Pro Ala Pro  
130 135 140

Pro Leu Leu Ala Asp Leu Gly Pro Ala Leu Glu Pro Glu Ser Pro Ala  
145 150 155 160

Ala Leu Gly Pro Pro Gly Tyr Leu His Ser Ala Pro Gly Pro Ala Pro  
165 170 175

Ala Pro Gly Glu Gly Pro Pro Pro Gly Thr Val Leu Glu Pro Gln Ser  
180 185 190

Ala Pro Glu Ser Ser Cys Pro Cys Arg Gly Ser Val Lys Asn Gln Pro  
195 200 205

Ser Glu Glu Leu Pro Asp Met Thr Thr Phe Pro Pro Arg Leu Leu Ala  
210 215 220

Glu Gln Leu Thr Leu Met Asp Ala Glu Leu Phe Lys Lys Val Val Leu  
225 230 235 240

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His Glu Cys Leu Gly Cys Ile Trp Gly Gln Gly His Leu Lys Gly Asn  
245 250 255

Glu His Met Ala Pro Thr Val Arg Ala Thr Ile Ala His Phe Asn Arg  
260 265 270

Leu Thr Asn Cys Ile Thr Thr Ser Cys Leu Gly Asp His Ser Met Arg  
275 280 285

Ala Arg Asp Arg Ala Arg Val Val Glu His Trp Ile Lys Val Ala Arg  
290 295 300

Glu Cys Leu Ser Leu Asn Asn Phe Ser Ser Val His Val Ile Val Ser  
305 310 315 320

Ala Leu Cys Ser Asn Pro Ile Gly Gln Leu His Lys Thr Trp Ala Gly  
325 330 335

Val Ser Ser Lys Ser Met Lys Glu Leu Lys Glu Leu Cys Lys Lys Asp  
340 345 350

Thr Ala Val Lys Arg Asp Leu Leu Ile Lys Ala Gly Ser Phe Lys Val  
355 360 365

Ala Thr Gln Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg Arg  
370 375 380

Gln Lys Lys Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu Leu  
385 390 395 400

Gln Arg Leu Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr Asn  
405 410 415

Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu Gln  
420 425 430

Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val Thr  
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PELLICER1A.ST25.txt

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1 5 10 15						
cgg ggt ggc tgg ggt gta act ggg gga gag gag gag agc ctc act gtc	Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu Ser Leu Thr Val	97				
20 25 30						
cct gtc gct gac acc tgg ca	Pro Val Ala Asp Thr Trp	117				
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## PELLICER1A.ST25.txt

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

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Arg	Gly	Gly	Trp	Gly	Val	Thr	Gly	Gly	Glu	Glu	Ser	Leu	Thr	Val
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Pro	Val	Ala	Asp	Thr	Trp
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&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

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agaagagaa	acagtctcag	ggaggcccgg	ctgcaagact	gggtgacaca	cacagggagt	180
gtggatctgg	gccagtgggg	cggggagctt	taaggtggcc	accaggaga	ggaaccccca	240
gagagtccag	atg	agg	ctg	cgg	agg	289
Met	Arg	Leu	Arg	Gln	Lys	Phe
1	5				10	

ctg	ggg	gat	ttt	ctg	act	gag	tta	cag	agg	ctg	gat	tcg	gcc	atc	ccg	337
Leu	Gly	Asp	Phe	Leu	Thr	Glu	Leu	Gln	Arg	Leu	Asp	Ser	Ala	Ile	Pro	
15				20						25						

gac	gac	ctg	gat	ggc	aac	acc	aac	aag	agg	agc	aag	gag	gtc	cga	gtt	385
Asp	Asp	Leu	Asp	Gly	Asn	Thr	Asn	Lys	Arg	Ser	Lys	Glu	Val	Arg	Val	
30				35					40				45			

ctg	cag	gaa	atg	cag	ctg	ctc	caa	gtg	gct	gcc	atg	aat	tac	agg	ctt	433
Leu	Gln	Glu	Met	Gln	Leu	Leu	Gln	Val	Ala	Ala	Met	Asn	Tyr	Arg	Leu	
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cg	cct	ctt	gag	aaa	ttt	gtc	acc	tat	ttc	aca	aga	atg	gag	cag	ctc	481
Arg	Pro	Leu	Glu	Lys	Phe	Val	Thr	Tyr	Phe	Thr	Arg	Met	Glu	Gln	Leu	
65				70						75						

agt	gac	aaa	gag	agc	tac	aag	ctg	tcc	tgc	cag	ctg	gag	ccc	gaa	aac	529
Ser	Asp	Lys	Glu	Ser	Tyr	Lys	Leu	Ser	Cys	Gln	Leu	Glu	Pro	Glu	Asn	
80				85						90						

ccg	taggctggca	acatcctgca	gtggctggga	acccacccggg	atgctggcca	582
Pro						

gaacacccggc	tctgcaccat	ccctcaccca	gaccgtagac	accagggAAC	cacatctagg	642
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aggctggcag	ctcagctgca	tcttgcctgt	gatcctcatc	accaactgct	cctgctggcc	702
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aggatcaggc	catgggactt	ttgtgagtca	ggcgggagac	cattttatgt	ttatTTTCTT	762
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PELLICER1A.ST25.txt

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Phe Leu Thr Glu Leu Gln Arg Leu Asp Ser Ala Ile Pro Asp Asp Leu  
 20 25 30

Asp Gly Asn Thr Asn Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu  
 35 40 45

Met Gln Leu Leu Gln Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu  
 50 55 60

Glu Lys Phe Val Thr Tyr Phe Thr Arg Met Glu Gln Leu Ser Asp Lys  
 65 70 75 80

Glu Ser Tyr Lys Leu Ser Cys Gln Leu Glu Pro Glu Asn Pro  
 85 90

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 <213> Homo sapiens

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 <222> (251)..(658)

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ctg ggg gat ttt ctg act gag tta cag agg ctg gat tcg gcc atc ccg Leu Gly Asp Phe Leu Thr Glu Leu Gln Arg Leu Asp Ser Ala Ile Pro 15 20 25	337
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PELLICER1A.ST25.txt

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cgg cct ctt gag aaa ttt gtc acc tat ttc aca aga atg gag cag ctc Arg Pro Leu Glu Lys Phe Val Thr Tyr Phe Thr Arg Met Glu Gln Leu 65 70 75	481
agt gac aaa gag agg ctg cac tgc agt gtc acc atc tct gtt cac tgc Ser Asp Lys Glu Arg Leu His Cys Ser Val Thr Ile Ser Val His Cys 80 85 90	529
aac gtc tgc ctt ctg ggc tca agt cct tcc tca gcc tcc caa gca gct Asn Val Cys Leu Leu Gly Ser Ser Pro Ser Ala Ser Gln Ala Ala 95 100 105	577
ggg act acc gct gta cac cac cat gtc cggttgcgttgttgc tac Gly Thr Thr Ala Val His His Val Arg Leu Phe Cys Cys Cys Tyr 110 115 120 125	625
aag ctg tcc tgc cag ctg gag ccc gaa aac ccgttaggctggca acatcctgca Lys Leu Ser Cys Gln Leu Glu Pro Glu Asn Pro 130 135	678
gtggctggga acccacccggg atgctggcca gaacaccggc tctgcaccat ccctcacccca gaccgttagac accagggAAC cacatctagg aggctggcag ctcagctgca tcttgccttg gatcctcatc accaactgct cctgctggcc aggtcagggc catgggactt ttgtgagtca ggcgggagac catttatgt ttatTTCTT tagtgtataa gtaagggttt tttcttaact ttcgttaaaa taaaattttt aaaaactatt caaaataaaaa aaaaaaaaaa 966	738 798 858 918

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<212> PRT  
<213> Homo sapiens

<400> 12

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20 25 30

Asp Gly Asn Thr Asn Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu  
35 40 45

Met Gln Leu Leu Gln Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu  
50 55 60

Glu Lys Phe Val Thr Tyr Phe Thr Arg Met Glu Gln Leu Ser Asp Lys  
65 70 75 80

Glu Arg Leu His Cys Ser Val Thr Ile Ser Val His Cys Asn Val Cys  
85 90 95

Leu Leu Gly Ser Ser Pro Ser Ser Ala Ser Gln Ala Ala Gly Thr Thr  
100 105 110

PELLICER1A.ST25.txt

Ala Val His His Val Arg Leu Phe Cys Cys Cys Tyr Lys Leu Ser  
115 120 125

Cys Gln Leu Glu Pro Glu Asn Pro  
130 . . . . . 135

<210> 13  
<211> 964  
<212> DNA  
<213> *Homo sapiens*

PELLICER1A.ST25.txt

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gcgggagACC attttatGTT tattttCTTt AGTGTATAAG taaggGTTT ttcttaactt	909
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20 25 30

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35 40 45

Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg Arg Gln Lys Lys  
50 55 60

Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu Leu Gln Arg Leu  
65 70 75 80

Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr Asn Lys Arg Ser  
85 90 95

Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu Gln Val Ala Ala  
100 105 110

Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val Thr Tyr Phe Thr  
115 120 125

Arg Met Glu Gln Leu Ser Asp Lys Glu Ser Tyr Lys Leu Ser Cys Gln  
130 135 140

Leu Glu Pro Glu Asn Pro  
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<222> (200)...(970)

<400> 15

## PELLICER1A.ST25.txt

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gtggatctgg gccagtggt atg agc acg gtg cca ggt ggc tcc cgc cac tcc Met Ser Thr Val Pro Gly Gly Ser Arg His Ser	232
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ctg ggg atc caa gtg cg 5 ggt ggc tgg ggt gta act ggg gga gag gag Leu Gly Ile Gln Val Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu	280
15 20 25	
gag agc ctc act gtc cct gtc gct gac acc tgg cag gcg ggg agc ttt Glu Ser Leu Thr Val Pro Val Ala Asp Thr Trp Gln Ala Gly Ser Phe	328
30 35 40	
aag gtg gcc acc cag gag agg aac ccc cag aga gtc cag atg agg ctg Lys Val Ala Thr Gln Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu	376
45 50 55	
cgg agg cag aag aag ggt gtg gtc ccc ttc ctg ggg gat ttt ctg act Arg Arg Gln Lys Lys Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr	424
60 65 70 75	
gag tta cag agg ctg gat tcg gcc atc ccg gac gac ctg gat ggc aac Glu Leu Gln Arg Leu Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn	472
80 85 90	
acc aac aag agg agc aag gag gtc cga gtt ctg cag gaa atg cag ctg Thr Asn Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu	520
95 100 105	
ctc caa gtg gct gcc atg aat tac agg ctt cgg cct ctt gag aaa ttt Leu Gln Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe	568
110 115 120	
gtc acc tat ttc aca aga atg gag cag ctc agt gac aaa gag agg ggg Val Thr Tyr Phe Thr Arg Met Glu Gln Leu Ser Asp Lys Glu Arg Gly	616
125 130 135	
ttt cac gat gat gtc cag gat cgt ctc aaa ctc ctg gcc tca agc aat Phe His Asp Asp Val Gln Asp Arg Leu Lys Leu Leu Ala Ser Ser Asn	664
140 145 150 155	
cca ccc acc tca gcc tcc caa agt act gac gtt aca ggt cta caa gct Pro Pro Thr Ser Ala Ser Gln Ser Thr Asp Val Thr Gly Leu Gln Ala	712
160 165 170	
gtc ctg cca gct gga gcc cga aaa ccc gta ggc tgg caa cat cct gca Val Leu Pro Ala Gly Ala Arg Lys Pro Val Gly Trp Gln His Pro Ala	760
175 180 185	
gtg gct ggg aac cca ccg gga tgc tgg cca gaa cac cgg ctc tgc acc Val Ala Gly Asn Pro Pro Gly Cys Trp Pro Glu His Arg Leu Cys Thr	808
190 195 200	
atc cct cac cca gac cgt aga cac cag gga acc aca tct agg agg ctg Ile Pro His Pro Asp Arg Arg His Gln Gly Thr Thr Ser Arg Arg Leu	856
205 210 215	
gca gct cag ctg cat ctt gcc ctg gat cct cat cac caa ctg ctc ctg Ala Ala Gln Leu His Leu Ala Leu Asp Pro His His Gln Leu Leu Leu	904
220 225 230 235	
ctg gcc agg atc agg cca tgg gac ttt tgt gag tca ggc ggg aga cca Leu Ala Arg Ile Arg Pro Trp Asp Phe Cys Glu Ser Gly Gly Arg Pro	952

## PELLICER1A.ST25.txt

240

245

250

ttt tat gtt tat ttt ctt tagtgtataa gtaagggttt tttcttaact 1000  
 Phe Tyr Val Tyr Phe Leu  
 255

ttcgttaaaa taaaattta aaaaactatt caaaataaaa aaaaaaaaaa 1048

<210> 16  
 <211> 257  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Met Ser Thr Val Pro Gly Gly Ser Arg His Ser Leu Gly Ile Gln Val  
 1 5 10 15

Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu Ser Leu Thr Val  
 20 25 30

Pro Val Ala Asp Thr Trp Gln Ala Gly Ser Phe Lys Val Ala Thr Gln  
 35 40 45

Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg Arg Gln Lys Lys  
 50 55 60

Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu Leu Gln Arg Leu  
 65 70 75 80

Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr Asn Lys Arg Ser  
 85 90 95

Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu Gln Val Ala Ala  
 100 105 110

Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val Thr Tyr Phe Thr  
 115 120 125

Arg Met Glu Gln Leu Ser Asp Lys Glu Arg Gly Phe His Asp Asp Val  
 130 135 140

Gln Asp Arg Leu Lys Leu Leu Ala Ser Ser Asn Pro Pro Thr Ser Ala  
 145 150 155 160

Ser Gln Ser Thr Asp Val Thr Gly Leu Gln Ala Val Leu Pro Ala Gly  
 165 170 175

Ala Arg Lys Pro Val Gly Trp Gln His Pro Ala Val Ala Gly Asn Pro  
 180 185 190

Pro Gly Cys Trp Pro Glu His Arg Leu Cys Thr Ile Pro His Pro Asp  
 195 200 205

## PELLICER1A.ST25.txt

Arg Arg His Gln Gly Thr Thr Ser Arg Arg Leu Ala Ala Gln Leu His  
210 215 220

Leu Ala Leu Asp Pro His His Gln Leu Leu Leu Leu Ala Arg Ile Arg  
225 230 235 240

Pro Trp Asp Phe Cys Glu Ser Gly Gly Arg Pro Phe Tyr Val Tyr Phe  
245 250 255

Leu

<210> 17  
<211> 1240  
<212> DNA  
<213> *Homo sapiens*

PELLICER1A.ST25.txt

tca cga tcatgtccag gatcgctca aactcctggc ctcaaggaaat ccacccacct	672
Ser Arg	
140	
cagcctccca aagtactgac gttacagggtg tgagccaccc cacctggcct agagaggctc	732
tcccgtaggc agctgcagag agcctatggc catgcctcca cggccagcat caagccctgt	792
tgcattggga ccactggggc cccaggattc cagctggca ggcactgaca ggggacctga	852
tgtgtggctc atggtggcct cacagctgct tctctgtcct gcctacaagc tgcctgcca	912
gctggagccc gaaaaccgtt aggctggcaa catcctgcag tggctggaa cccaccggaa	972
tgctggccag aacaccggct ctgcaccatc cctcaccagg accgtagaca ccagggaaac	1032
cacatctagg aggctggcag ctcagctgca tcttgccctg gatcctcatc accaactgct	1092
cctgctggcc aggatcaggc catggactt ttgtgagtca ggcggagac cattttatgt	1152
ttatTTTCTT tagtgtataa gtaagggttt ttcttaact ttcttaaaa taaaatttttta	1212
aaaaactatt caaaataaaa aaaaaaaaaaaaa	1240

<210> 18

<211> 141

<212> PRT

<213> Homo sapiens

<400> 18

Met Ser Thr Val Pro Gly Gly Ser Arg His Ser Leu Gly Ile Gln Val  
 1 5 10 15

Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu Glu Ser Leu Thr Val  
 20 25 30

Pro Val Ala Asp Thr Trp Gln Ala Gly Ser Phe Lys Val Ala Thr Gln  
 35 40 45

Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg Arg Gln Lys Lys  
 50 55 60

Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu Leu Gln Arg Leu  
 65 70 75 80

Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr Asn Lys Arg Ser  
 85 90 95

Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu Gln Val Ala Ala  
 100 105 110

Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val Thr Tyr Phe Thr  
 115 120 125

Arg Met Glu Gln Leu Ser Asp Lys Glu Gly Val Ser Arg  
 130 135 140

## PELLICER1A.ST25.txt

<210> 19  
<211> 529  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (14)..(463)

<400> 19  
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Met Ser Thr Val Pro Gly Gly Ser Arg His Ser Leu  
1 5 10

ggg atc caa. gtg cg<sup>15</sup> ggt ggc tgg ggt gta act ggg gga gag gag gag  
 Gly Ile Gln Val Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu Glu Glu 97  
 15 20 25

agc ctc act gtc cct gtc gct gac acc tgg cag gcg ggg agc ttt aag 145  
Ser Leu Thr Val Pro Val Ala Asp Thr Trp Gln Ala Gly Ser Phe Lys  
30 35 40

gtg gcc acc cag gag agg aac ccc cag aga gtc cag atg agg ctg cgg 193  
 Val Ala Thr Gln Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg  
 45 50 55 60

agg cag aag aag ggt gtg gtc ccc ttc ctg ggg gat ttt ctg act gag 241  
 Arg Gln Lys Lys Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu  
           65           70           75

tta cag agg ctg gat tcg gcc atc ccg gac gac ctg gat ggc aac acc 289  
 Leu Gln Arg Leu Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr  
           80          85          90

aac aag agg agc aag gag gtc cga gtt ctg cag gaa atg cag ctg ctc 337  
 Asn Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu  
 95 100 105

caa gtg gct gcc atg aat tac agg ctt cg<sup>g</sup> cct ctt gag aaa tt<sup>t</sup> gtc      385  
 Gln Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val  
 110            115            120

acc tat ttc aca aga atg gag cag ctc agt gac aaa gag agc tac aag 433  
 Thr Tyr Phe Thr Arg Met Glu Gln Leu Ser Asp Lys Glu Ser Tyr Lys  
 125 130 135 140

ctg tcc tgc cag ctg gag ccc gaa aac ccg tagggttttt tcttaacttt 483  
 Leu Ser Cys Gln Leu Glu Pro Glu Asn Pro  
                  145                 150

cgttaaaata aaattttaaa aaactattca aaataaaaaaa aaaaaaa - 529

<210> 20  
<211> 150  
<212> PRT  
<213> *Homo sapiens*

<400> 20

Met Ser Thr Val Pro Gly Gly Ser Arg His Ser Leu Gly Ile Gln Val  
1 5 10 15

Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu Glu Ser Leu Thr Val  
20 25 30

PELLICER1A.ST25.txt

Pro Val Ala Asp Thr Trp Gln Ala Gly Ser Phe Lys Val Ala Thr Gln  
 35 40 45

Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg Arg Gln Lys Lys  
 50 55 60

Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu Leu Gln Arg Leu  
 65 70 75 80

Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr Asn Lys Arg Ser  
 85 90 95

Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu Gln Val Ala Ala  
 100 105 110

Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val Thr Tyr Phe Thr  
 115 120 125

Arg Met Glu Gln Leu Ser Asp Lys Glu Ser Tyr Lys Leu Ser Cys Gln  
 130 135 140

Leu Glu Pro Glu Asn Pro  
 145 150

<210> 21  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (181)..(462)

<400> 21  
 tgagggtgct cgtgcctggt tcttcctcag agggatgacg gtgagaacaa cggcaacagc 60  
 tacaggaaac tgagccctca gaggccctgt gaggtagctg tggtttgcatt cactctttac 120  
 agaagagggg cggggagctt taaggtggcc acccaggaga ggaaccccca gagagtccag 180  
 atg agg ctg cgg agg cag aag aag ggt gtg gtc ccc ttc ctg ggg gat 228  
 Met Arg Leu Arg Arg Gln Lys Lys Gly Val Val Pro Phe Leu Gly Asp  
 1 5 10 15

ttt ctg act gag tta cag agg ctg gat tcg gcc atc ccg gac gac ctg 276  
 Phe Leu Thr Glu Leu Gln Arg Leu Asp Ser Ala Ile Pro Asp Asp Leu  
 20 25 30

gat ggc aac acc aac aag agg agc aag gag gtc cga gtt ctg cag gaa 324  
 Asp Gly Asn Thr Asn Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu  
 35 40 45

atg cag ctg ctc caa gtg gct gcc atg aat tac agg ctt cgg cct ctt 372  
 Met Gln Leu Leu Gln Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu  
 50 55 60

gag aaa ttt gtc acc tat ttc aca aga atg gag cag ctc agt gac aaa 420

## PELLICER1A.ST25.txt

Glu Lys Phe Val Thr Tyr Phe Thr Arg Met Glu Gln Leu Ser Asp Lys  
 65 70 75 80

gag agc tac aag ctg tcc tgc cag ctg gag ccc gaa aac ccg 462  
 Glu Ser Tyr Lys Leu Ser Cys Gln Leu Glu Pro Glu Asn Pro  
 85 90

taggctggca acatcctgca gtggctggga acccaccggg atgctggcca gaacaccggc 522  
 tctgcaccat ccctcaccca gacccgtaga caccaggaa ccacatctag gaggctggca 582  
 gctcagctgc atcttgcctt ggatcctcat caccaactgc tcctgctggc caggatcagg 642  
 ccatggact tttgtgagtc aggcccggaga ccattttatg tttatttct ttagtgtata 702  
 agtaagggtt ttttcttaac ttctgttaaa ataaaatttt aaaaaactat tcaaaataaa 762  
 aaaaaaaaaa 771

<210> 22  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 22

Met Arg Leu Arg Arg Gln Lys Lys Gly Val Val Pro Phe Leu Gly Asp  
 1 5 10 15

Phe Leu Thr Glu Leu Gln Arg Leu Asp Ser Ala Ile Pro Asp Asp Leu  
 20 25 30

Asp Gly Asn Thr Asn Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu  
 35 40 45

Met Gln Leu Leu Gln Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu  
 50 55 60

Glu Lys Phe Val Thr Tyr Phe Thr Arg Met Glu Gln Leu Ser Asp Lys  
 65 70 75 80

Glu Ser Tyr Lys Leu Ser Cys Gln Leu Glu Pro Glu Asn Pro  
 85 90

<210> 23  
 <211> 1044  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (196)..(966)

<400> 23  
 gggtgctcggt gcctgggtct tcctcagagg gatgacgggt agaacaaggc aacagctaca 60  
 ggaaactgag ccctcagagg ccctgtgagg tagctgtggt ttgcatcaact ctttacagaa 120  
 gagggaaacag tctcaggag gccccggctgc aagactgggt gacacacaca gggagtgtgg 180

## PELLICER1A.ST25.txt

atctggcca gtgg atg agc acg gtg cca ggt ggc tcc cgc cac tcc ctg Met Ser Thr Val Pro Gly Gly Ser Arg His Ser Leu 1 5 10	231
ggg atc caa gtg cggt ggc tgg ggt gta act ggg gga gag gag gag Gly Ile Gln Val Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu Glu 15 20 25	279
agc ctc act gtc cct gtc gct gac acc tgg cag gcg ggg agc ttt aag Ser Leu Thr Val Pro Val Ala Asp Thr Trp Gln Ala Gly Ser Phe Lys 30 35 40	327
gtg gcc acc cag gag agg aac ccc cag aga gtc cag atg agg ctg cgg Val Ala Thr Gln Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg 45 50 55 60	375
agg cag aag aag ggt gtg gtc ccc ttc ctg ggg gat ttt ctg act gag Arg Gln Lys Lys Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu 65 70 75	423
tta cag agg ctg gat tcg gcc atc ccg gac gac ctg gat ggc aac acc Leu Gln Arg Leu Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr 80 85 90	471
aac aag agg agc aag gag gtc cga gtt ctg cag gaa atg cag ctg ctc Asn Lys Arg Ser Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu 95 100 105	519
caa gtg gct gcc atg aat tac agg ctt cgg cct ctt gag aaa ttt gtc Gln Val Ala Ala Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val 110 115 120	567
acc tat ttc aca aga atg gag cag ctc agt gac aaa gag aga tgg ggt Thr Tyr Phe Thr Arg Met Glu Gln Leu Ser Asp Lys Glu Arg Trp Gly 125 130 135 140	615
ttc acg atg atg tcc agg atc gtc tca aac tcc tgg cct caa gca atc Phe Thr Met Met Ser Arg Ile Val Ser Asn Ser Trp Pro Gln Ala Ile 145 150 155	663
cac cca cct cag cct ccc aaa gta ctg acg tta cag cta caa gct gtc His Pro Pro Gln Pro Pro Lys Val Leu Thr Leu Gln Leu Gln Ala Val 160 165 170	711
ctg cca gct gga gcc cga aaa ccc gta ggc tgg caa cat cct gca gtg Leu Pro Ala Gly Ala Arg Lys Pro Val Gly Trp Gln His Pro Ala Val 175 180 185	759
gct ggg aac cca ccg gga tgc tgg cca gaa cac cgg ctc tgc acc atc Ala Gly Asn Pro Pro Gly Cys Trp Pro Glu His Arg Leu Cys Thr Ile 190 195 200	807
cct cac cca gac cgt aga cac cag gga acc aca tct agg agg ctg gca Pro His Pro Asp Arg Arg His Gln Gly Thr Thr Ser Arg Arg Leu Ala 205 210 215 220	855
gct cag ctg cat ctt gcc ctg gat cct cat cac caa ctg ctc ctg ctg Ala Gln Leu His Leu Ala Leu Asp Pro His His Gln Leu Leu Leu Leu 225 230 235	903
gcc agg atc agg cca tgg gac ttt tgt gag tca ggc ggg aga cca ttt Ala Arg Ile Arg Pro Trp Asp Phe Cys Glu Ser Gly Gly Arg Pro Phe 240 245 250	951
tat gtt tat ttt ctt tagtgtataa gtaagggttt tttcttaact ttcgtaaaa Tyr Val Tyr Phe Leu 255	1006

taaaatttta aaaaactatt caaaataaaa aaaaaaaaa

1044

<210> 24  
<211> 257  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 24

Met Ser Thr Val Pro Gly Gly Ser Arg His Ser Leu Gly Ile Gln Val  
1 5 10 15

Arg Gly Gly Trp Gly Val Thr Gly Gly Glu Glu Glu Ser Leu Thr Val  
20 25 30

Pro Val Ala Asp Thr Trp Gln Ala Gly Ser Phe Lys Val Ala Thr Gln  
35 40 45

Glu Arg Asn Pro Gln Arg Val Gln Met Arg Leu Arg Arg Gln Lys Lys  
50 55 60

Gly Val Val Pro Phe Leu Gly Asp Phe Leu Thr Glu Leu Gln Arg Leu  
65 70 75 80

Asp Ser Ala Ile Pro Asp Asp Leu Asp Gly Asn Thr Asn Lys Arg Ser  
85 90 95

Lys Glu Val Arg Val Leu Gln Glu Met Gln Leu Leu Gln Val Ala Ala  
100 105 110

Met Asn Tyr Arg Leu Arg Pro Leu Glu Lys Phe Val Thr Tyr Phe Thr  
115 120 125

Arg Met Glu Gln Leu Ser Asp Lys Glu Arg Trp Gly Phe Thr Met Met  
130 135 140

Ser Arg Ile Val Ser Asn Ser Trp Pro Gln Ala Ile His Pro Pro Gln  
145 150 155 160

Pro Pro Lys Val Leu Thr Leu Gln Leu Gln Ala Val Leu Pro Ala Gly  
165 170 175

Ala Arg Lys Pro Val Gly Trp Gln His Pro Ala Val Ala Gly Asn Pro  
180 185 190

Pro Gly Cys Trp Pro Glu His Arg Leu Cys Thr Ile Pro His Pro Asp  
195 200 205

Arg Arg His Gln Gly Thr Thr Ser Arg Arg Leu Ala Ala Gln Leu His  
210 215 220

Leu Ala Leu Asp Pro His His Gln Leu Leu Leu Ala Arg Ile Arg  
225 230 235 240

PELLICER1A.ST25.txt

Pro Trp Asp Phe Cys Glu Ser Gly Gly Arg Pro Phe Tyr Val Tyr Phe  
245 250 255

Leu

<210> 25  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic

<400> 25  
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21

<210> 26  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic

<400> 26  
gucucuugca ggcgacaaat t

21

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic

<400> 27  
uuacaggccuu cggccucuut t

21

<210> 28  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic

<400> 28  
aagaggccga agccuguaat t

21